EXHIBIT D: CLEAN VERSION OF PENDING CLAIMS
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(ATTORNEY DOCKET NO. 9301-123)

(as amended January 9, 2001)

1. A method for analyzing exon expression in a cell sample, comprising measuring the expression levels of a plurality of individual exons or multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived, wherein the measured expression level of each exon or multiexon is not averaged with the measured expression level of one or more different exons or multiexons in the same gene; thereby analyzing the exon expression of said cell sample.

2. The method of claim 1, wherein said measured expression levels are used to determine a distinguishing structural characteristic of an expressed variant for each of one or more of said exons or multiexons.

3. The method of claim 2, wherein the structural characteristic of said expressed variant for each of one or more of said exons or multiexons is determined by determining the length of said expressed variant.

4. The method of claim 1, wherein said plurality of individual exons or multiexons consists of at least 3 different exons or multiexons.

5. The method of claim 1, wherein said plurality of individual exons or multiexons consists of at least 5 different exons or multiexons.

6. The method of claim 1, wherein said plurality of individual exons or multiexons consists of at least two different exons.

7. The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 100 different genes.

8. The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 1,000 different genes.

9. The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 10,000 different genes.

10. (Amended) The method of claim 1, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

11. The method of claim 10, wherein said plurality of individual exons or multiexons consists of at least 3 different exons.

12. The method of claim 10, wherein said plurality of individual exons or multiexons consists of at least 5 different exons.

13. The method of claim 10, 11 or 12, wherein said plurality of different genes consists of at least 1,000 different genes.

14. The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

15. The method of claim 10, wherein said plurality of polynucleotide probes consists

of at least 1,000 different polynucleotide probes.

16. The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

17. The method of claim 10, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

18. The method of claim 10, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

19. The method of claim 10, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

20. The method of claim 10, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

21. The method of claim 10, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

22. The method of claim 10, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

23. The method of claim 10, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

24. The method of claim 10, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

25. The method of claim 10, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

26. The method of claim 10, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

27. The method of claim 10, wherein each of said different nucleotide sequences consists of 60 nucleotides.

28. The method of claim 10, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

29. The method of claim 28, wherein said linker sequence comprises a linker sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

30. The method of claim 10, wherein said sequence is complementary to the sequence of a full length exon.

31. The method of claim 10, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

32. The method of claim 31, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

33. The method of claim 31, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

34. The method of claim 10, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

35. The method of claim 1 or 10, wherein said expression levels are measured as continuous variables.

36. The method of claim 35, wherein said expression levels are measured as continuous variables and represented as absolute abundance.

45. (Amended) The method of claim 1 or 10, wherein said organism is a human.

46. (Amended) The method of claim 1 or 10, wherein said organism is a plant.

86. (Amended) The method of claim 1 or 10, wherein said cell sample has been subjected to a perturbation.

87. The method of claim 86, wherein said organism is a human.

88. The method of claim 86, wherein said organism is a plant.

89. The method of claim 86, further comprising comparing the expression levels of at least a portion of said plurality of individual exons or multiexons in said cell sample having been subjected to said perturbation with the expression level of said portion of said plurality of individual exons or multiexons in a cell sample of the same type not having been subjected to said perturbation.

90. The method of claim 89, wherein said comparing comprises determining the difference between the expression level of each exon or multiexon in said portion of said plurality of individual exons or multiexons in said cell sample having been subjected to said perturbation and the expression level of the corresponding exons or multiexons in said cell sample of the same type not having been subjected to said perturbation.

157. (Amended) The method of claim 1, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a

sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

158. The method of claim 157, wherein said plurality of individual exons or multiexons consists of at least 3 different exons.

159. The method of claim 157, wherein said plurality of individual exons or multiexons consists of at least 5 different exons.

160. The method of claim 157, 158 or 159, wherein said plurality of different genes consists of at least 1,000 different genes.

161. The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

162. The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

163. The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

164. The method of claim 157, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

165. The method of claim 157, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

166. The method of claim 157, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

167. The method of claim 157, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

168. The method of claim 157, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

169. The method of claim 157, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

170. The method of claim 157, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

171. The method of claim 157, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

172. The method of claim 157, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

173. The method of claim 157, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

174. The method of claim 157, wherein each of said different nucleotide sequences consists of 60 nucleotides.

175. The method of claim 157, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

176. The method of claim 175, wherein said linker sequence comprises a spacer sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

177. The method of claim 157, wherein said sequence is complementary to the sequence of a full length exon.

178. The method of claim 157, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

179. The method of claim 178, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

180. The method of claim 178, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

181. The method of claim 157, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

182. (Amended) The method of claim 157, wherein said expression levels are measured as continuous variables.

183. The method of claim 182, wherein said expression levels are measured as continuous variables and represented as absolute abundance.

212. (Amended) The method of claim 1 or 10, wherein said organism is a fungus.

213. The method of claim 86, wherein said organism is a fungus.

214. (New) The method of claim 2, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

215. (New) The method of claim 214, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

216. (New) The method of claim 214, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a sequence spanning the splice junction between different exons in a multiexon.

217. (New) The method of claim 216, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

218. (New) The method of any one of claims 214-217, wherein said plurality of different genes consists of at least 1,000 different genes.

219. (New) The method of any one of claims 214-217, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

220. (New) The method of claim 219, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

221. (New) The method of claim 220, wherein each of said different nucleotide sequences consists of 40 to 70 nucleotides.

222. (New) The method of claim 221, wherein each of said different nucleotide sequences consists of 60 nucleotides.

223. (New) The method of any one of claims 214-217, wherein said organism is a human.

224. (New) The method of any one of claims 214-217, wherein said organism is a plant.

225. (New) The method of any one of claims 214-217, wherein said cell sample has been subjected to a perturbation.

226. (New) The method of claim 3, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

227. (New) The method of claim 226, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

228. (New) The method of claim 226, wherein at least one of said plurality of

polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a sequence spanning the splice junction between different exons in a multiexon.

229. (New) The method of claim 228, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

230. (New) The method of any one of claims 226-229, wherein said plurality of different genes consists of at least 1,000 different genes.

231. (New) The method of any one of claims 226-229, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

232. (New) The method of claim 231, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

233. (New) The method of claim 232, wherein each of said different nucleotide sequences consists of 40 to 70 nucleotides.

234. (New) The method of claim 233, wherein each of said different nucleotide sequences consists of 60 nucleotides.

235. (New) The method of any one of claims 226-229, wherein said organism is a human.

236. (New) The method of any one of claims 226-229, wherein said organism is a plant.

237. (New) The method of any one of claims 226-229, wherein said cell sample has been subjected to a perturbation.

238. (New) The method of claim 2, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

239. (New) The method of claim 238, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

240. (New) The method of claim 238, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a sequence spanning the splice junction between different exons in a multiexon.

241. (New) The method of claim 240, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and

hybridizable to different introns of said plurality of genes in the genome of said organism.

242. (New) The method of any one of claims 238-241, wherein said plurality of different genes consists of at least 1,000 different genes.

243. (New) The method of any one of claims 238-241, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

244. (New) The method of claim 243, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

245. (New) The method of claim 244, wherein each of said different nucleotide sequences consists of 40 to 70 nucleotides.

246. (New) The method of claim 245, wherein each of said different nucleotide sequences consists of 60 nucleotides.

247. (New) The method of any one of claims 238-241, wherein said organism is a human.

248. (New) The method of any one of claims 238-241, wherein said organism is a plant.

249. (New) The method of any one of claims 238-241, wherein said cell sample has been subjected to a perturbation.

250. (New) The method of claim 3, wherein said measuring is performed by a method

comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived; and

(b) measuring levels of hybridization between said probes and said RNAs or nucleic acids.

251. (New) The method of claim 250, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

252. (New) The method of claim 250, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a sequence spanning the splice junction between different exons in a multiexon.

253. (New) The method of claim 252, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

254. (New) The method of any one of claims 250-253, wherein said plurality of different genes consists of at least 1,000 different genes.

255. (New) The method of any one of claims 250-253, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

256. (New) The method of claim 255, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

257. (New) The method of claim 256, wherein each of said different nucleotide sequences consists of 40 to 70 nucleotides.

258. (New) The method of claim 257, wherein each of said different nucleotide sequences consists of 60 nucleotides.

259. (New) The method of any one of claims 250-253, wherein said organism is a human.

260. (New) The method of any one of claims 250-253, wherein said organism is a plant.

261. (New) The method of any one of claims 250-253, wherein said cell sample has been subjected to a perturbation.

262. (New) The method of any one of claims 214-217, 226-229, 238-241 and 250-253, wherein said organism is a fungus.

263. (New) The method of any one of claims 214-217, 226-229, 238-241 and 250-253, wherein said array of polynucleotide probes further comprises one or more sets of successive overlapping probes tiled along the longest variant of an exon.

264. (New) The method of any one of claims 216, 228, 240 and 252, wherein said array of polynucleotide probes further comprises variant junction probes, wherein each of said variant junction probes is specifically hybridizable to a sequence spanning the splice junction between a different variant of an exon and a neighboring exon.

265. (New) The method of claim 86, wherein said perturbation is exposure to a drug.

266. (New) The method of claim 86, wherein said perturbation is a genetic mutation.

267. (New) The method of claim 86, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.

268. (New) The method of claim 225, wherein said perturbation is exposure to a drug.

269. (New) The method of claim 225, wherein said perturbation is a genetic mutation.

270. (New) The method of claim 225, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.

271. (New) The method of claim 237, wherein said perturbation is exposure to a drug.

272. (New) The method of claim 237, wherein said perturbation is a genetic mutation.

273. (New) The method of claim 237, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.

274. (New) The method of claim 249, wherein said perturbation is exposure to a drug.

275. (New) The method of claim 249, wherein said perturbation is a genetic mutation.

276. (New) The method of claim 249, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.

277. (New) The method of claim 261, wherein said perturbation is exposure to a drug.

278. (New) The method of claim 261, wherein said perturbation is a genetic mutation.

279. (New) The method of claim 261, wherein said perturbation comprises mutation of one or more genes and exposure to a drug.